APPLICANTS COPY

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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:   July 28, 2004, 11:26:10 ; Search time 14 Seconds
                           (without alignments)
                799.649 Million cell updates/sec

Title:          US-10-028-072-4
Perfect score:  1132
Sequence:       1 MVSMSFKRNRSDRFYSTRCC.........PEIAVYPAFESTSSVRFANL 215

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:       141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1087	96.0	233	1	MTRP_HUMAN	Q15012 homo sapien
2	1061	93.7	233	1	MTRP_MOUSE	Q60961 mus musculu
3	191	16.9	262	1	LAM5_HUMAN	Q13571 homo sapien
4	189.5	16.7	261	1	LAM5_MOUSE	Q61168 mus musculu
5	103.5	9.1	385	1	G22C_DROME	P58952 drosophila
6	93	8.2	413	1	Y567_BUCAP	Q8K902 buchnera ap
7	90	8.0	274	1	NU2M_DROMA	P29867 drosophila
8	89.5	7.9	446	1	D3DR_MOUSE	P30728 mus musculu
9	89.5	7.9	446	1	D3DR_RAT	P19020 rattus norv
10	88	7.8	551	1	FIXN_AZOCA	P98056 azorhizobiu
11	87.5	7.7	432	1	Y672_METJA	Q58086 methanococc
12	87.5	7.7	535	1	YDW6_SCHPO	O13912 schizosacch
13	87	7.7	341	1	NU2M_DROME	P03896 drosophila
14	87	7.7	2253	1	PKDR_HUMAN	Q9ntg1 homo sapien
15	86.5	7.6	112	1	YUW4_CAEEL	Q20263 caenorhabdi
16	86.5	7.6	1163	1	KCH2_RAT	Q08962 rattus norv
17	85.5	7.6	341	1	NU2M_DROYA	P03895 drosophila
18	85.5	7.6	341	1	NU2M_DROME	Q9t5b7 drosophila
19	85.5	7.6	457	1	YG90_HABIN	P45320 haemophilus
20	85.5	7.6	570	1	NU5M_PARTE	P15584 paramecium
21	85	7.5	570	1	CYB_CAMBA	Q34028 camelus bac
22	85	7.5	695	1	CIQ4_HUMAN	P56696 homo sapien
23	85	7.5	267	1	CYB_AKOCU	P48518 akodon curs
24	84.5	7.5	379	1	CYB_FERAT	Q9tdn1 feresa atte
25	84.5	7.5	379	1	CYB_KOBEL	O99342 kobus ellip
26	84.5	7.5	379	1	CYB_MUNMU	Q9cdq7 munticus m
27	84.5	7.5	379	1	CYB_ZIPCA	Q36262 ziphius cav
28	84.5	7.5	590	1	NU5M_TRYBB	P04540 trypanosoma
29	84.5	7.5	1159	1	KCH2_HUMAN	Q12809 homo sapien
30	84.5	7.5	1162	1	KCH2_MOUSE	O35109 mus musculu
31	84	7.4	379	1	CYB_VBSMU	Q957c8 vespertilio
32	83.5	7.4	379	1	CYB_BUBBU	Q33950 bubalus bub
33	83.5	7.4	379	1	CYB_BUBDE	P92870 bubalus dep
34	83.5	7.4	379	1	CYB_BUBQU	P92592 bubalus qua
35	83.5	7.4	379	1	CYB_MYONA	Q95629 myotis natt
36	83.5	7.4	423	1	GP83_MOUSE	P30731 mus musculu
37	83	7.3	379	1	CYB_PTEHP	Q8sj24 pteropus hy
38	83	7.3	470	1	MTR_NEUCR	P38680 neurospora
39	83	7.3	783	1	YAF3_YEAST	P39719 saccharomyc
40	82.5	7.3	274	1	NU2M_DROSE	P29868 drosophila
41	82.5	7.3	274	1	NU2M_DROSI	P29869 drosophila
42	82.5	7.3	380	1	CYB_APOSE	Q9t917 apogon semi
43	82.5	7.3	380	1	CYB_NEORH	Q8hib9 neocyttus r
44	82.5	7.3	380	1	CYB_POLOR	Q95920 polypterus
45	82	7.2	300	1	NU2M_ASCSU	P24877 ascaris suu

ALIGNMENTS

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RESULT 1
MTRP_HUMAN
ID   MTRP_HUMAN     STANDARD;     PRT;    233 AA.
AC   Q15012;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane
DE   spanning transporter MTP).
GN   LAPTM4A OR MTRP OR KIAA0108.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95308325; PubMed=7788527;
RA   Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA   Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. III.
RT   The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT   analysis of cDNA clones from human cell line KG-1.";
RL   DNA Res. 2:37-43(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May function in the transport of nucleosides and/or
CC       nucleoside derivatives between the cytosol and the lumen of an
CC       intracellular membrane-bound compartment (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. May reside in an
CC       intracellular membrane-bound compartment (Potential).
CC   -!- DOMAIN: The C-terminal domain is necessary for retention within
CC       intracellular membranes (By similarity).
```

DR   EMBL; D14696; BAA03522.1; -.
DR   EMBL; BC000421; AAH00421.1; -.
DR   Genew; HGNC:6924; LAPTM4A.
DR   InterPro; IPR004687; Mtp.
DR   Pfam; PF03821; Mtp; 1.
DR   TIGRFAMs; TIGR00799; mtp; 1.
KW   Transmembrane; Transport.
FT   TRANSMEM   29   49   POTENTIAL.
FT   TRANSMEM   82   102   POTENTIAL.
FT   TRANSMEM   108   128   POTENTIAL.
FT   TRANSMEM   160   180   POTENTIAL.
FT   DOMAIN   226   229   POLY-PRO.
SQ   SEQUENCE   233 AA; 26800 MW; 9BB76152B6E1365E CRC64;

Query Match   96.0%; Score 1087; DB 1; Length 233;
Best Local Similarity   99.5%; Pred. No. 1.6e-78;
Matches 205; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MVSMSFKRNRSDRFYSTRCCGCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVSMSFKRNRSDRFYSTRCCGCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAV 60

Qy   61 NIQYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NIQYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDF 120

Qy   121 VLSCLVAISSLTYLPRIKEYLDQLPDPFYKDDLLALDSSCLLFIVLVFFALFIIFKAYLI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 VLSCLVAISSLTYLPRIKEYLDQLPDPFYKDDLLALDSSCLLFIVLVFFALFIIFKAYLI 180

Qy   181 NCVWNCYKYINNRNVPEIAVYPAFES 206
              ||||||||||||||||||||||||||
Db   181 NCVWNCYKYINNRNVPEIAVYPAFEA 206

RESULT 2
MTRP_MOUSE
ID   MTRP_MOUSE   STANDARD;   PRT;   233 AA.
AC   Q60961;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Lysosomal-associated transmembrane protein 4A (Golgi 4-transmembrane
DE   spanning transporter) (Mouse transporter protein) (MTP).
GN   LAPTM4A OR MTRP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2; TISSUE=Brain, and Leukemia;
RX   MEDLINE=96199248; PubMed=8621662;
RA   Hogue D.L., Ellison M.J., Young J.D., Cass C.E.;
RT   "Identification of a novel membrane transporter associated with
RT   intracellular membranes by phenotypic complementation in the yeast
RT   Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 271:9801-9808(1996).
CC   -!- FUNCTION: May function in the transport of nucleosides and/or
CC   nucleoside derivatives between the cytosol and the lumen of an
CC   intracellular membrane-bound compartment. May reside in an
CC   intracellular membrane-bound compartment (Potential). Isoform
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. May possibly be localized in the plasma membrane.

CC   Event=Alternative initiation;
CC   Comment=2 isoforms, Long (shown here) and Short/Truncated/MTP1,
CC   may be produced by alternative initiation;
CC   -!- DOMAIN: The C-terminal domain is necessary for retention within
CC   intracellular membranes.
DR   EMBL; U34259; AAB04938.1; -.
DR   MGD; MGI:1108017; Laptm4a.
DR   InterPro; IPR004687; Mtp.
DR   Pfam; PF03821; Mtp; 1.
DR   TIGRFAMs; TIGR00799; mtp; 1.
KW   Transmembrane; Transport; Alternative initiation.
FT   CHAIN   1   233   LYSOSOMAL-ASSOCIATED TRANSMEMBRANE
FT   PROTEIN 4A, ISOFORM LONG.
FT   CHAIN   90   233   LYSOSOMAL-ASSOCIATED TRANSMEMBRANE
FT   PROTEIN 4A, ISOFORM SHORT.
FT   INIT_MET   90   90   FOR ISOFORM SHORT.
FT   TRANSMEM   29   49   POTENTIAL.
FT   TRANSMEM   82   102   POTENTIAL.
FT   TRANSMEM   108   128   POTENTIAL.
FT   TRANSMEM   160   180   POTENTIAL.
FT   DOMAIN   226   229   POLY-PRO.
SQ   SEQUENCE   233 AA; 26857 MW; CA409AC77ACB4D6E CRC64;

Query Match   93.7%; Score 1061; DB 1; Length 233;
Best Local Similarity   97.1%; Pred. No. 1.7e-76;
Matches 200; Conservative   4; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MVSMSFKRNRSDRFYSTRCCGCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAV 60
              ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MVSMTFKRSRSDRFYSTRCCGCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAV 60

Qy   61 NIQYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NIQYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDP 120

Qy   121 VLSCLVAISSLTYLPRIKEYLDQLPDPFYKDDLLALDSSCLLFIVLVFFALFIIFKAYLI 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| :||||||||
Db   121 VLSCLVAISSLTYLPRIKEYLDQLPDPFYKDDLLALDSSCLLFIVLVFFVFFVVFIIFKAYLI 180

Qy   181 NCVWNCYKYINNRNVPEIAVYPAFES 206
              ||||||||||||||||||||||||||
Db   181 NCVWNCYKYINNRNVPEIAVYPAFET 206